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Result
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Maximum DB
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Perfect score:
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                                                                                                                   1090
1088.5
1086
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1: /cgn2_6/ptodata/1/paa/U
2: /cgn2_6/ptodata/1/paa/U
3: /cgn2_6/ptodata/1/paa/U
4: /cgn2_6/ptodata/1/paa/U
5: /cgn2_6/ptodata/1/paa/U
6: /cgn2_6/ptodata/1/paa/U
7: /cgn2_6/ptodata/1/paa/U
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 ,
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/cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US00_NEW_COMB.pep:*
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              US-09-502-984B-1
US-09-791-537-39806
US-09-791-537-38134
US-09-791-537-68105
US-09-791-537-67299
US-09-502-984B-12
US-09-502-984B-12
US-09-502-984B-13
US-09-502-984B-13
US-09-502-984B-11
US-09-502-984B-3
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67299, A
2, Appli
86927, A
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38134, A
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US-09-502-984B-1
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APPLICANT: Luo, Peizhi
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Best Local Similarity
Matches 225; Conserv
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17.2	70.9	71.3	80.9	80.9	82.2	82.3	82.3	87.9	88.8	88.8	88.9	89.7	89.8	89.8	89.9	90.1	90.2
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Sequence 34, Appl	4.0	Sequence 40030,	Sequence 55613,	Sequence 4913, Ap	Sequence 9845,	Sequence 126514,	Sequence 1440, Ap		Sequence 37, App	Sequence 6, Appl	27,	-	Sequence 26, Appl	Sequence 22, App	Sequence 23, App	Sequence 25, App	Sequence 24, App

## ALIGNMENTS

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TITLE OF INVENTION: STRUCTURE-BASED SCREENING TEN FILE REFERENCE: A-68126-1/RPT/RMS/RMK CURRENT APPLICATION UNMBER: US/09/502,984B CURRENT FILING DATE: 2000-02-11 PRIOR PELLING DATE: 1999-02-11 PRIOR FILING DATE: 1999-02-11 PRIOR FILING DATE: 1999-02-11 PRIOR FILING DATE: 1999-04-29 PRIOR FILING DATE: 1999-04-29 NUMBER OF SEQ ID NOS: 37 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1

LENGTH: 225
US-09-791-537-99806; Application US/09791537; Sequence 99806, Application US/09791537; GENERAL INFORMATION: APPLICANT: Bionomix, Inc.; APPLICANT: Debe, Derek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; ORGANISM: Homo sapiens US-09-502-984B-1
                                                                                                                                                                                                181 CVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSDLD 225
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100.0%; Pred. No. 2.7e-106;
tive 0; Mismatches 0;
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US-09-791-537-38134
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S-09-791-537-38134
Sequence 38134, Application US/09791537
GENERAL INFORMATION:
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOCTWARE: Patentin version 3.0
SEQ ID NO 38134
LENGTH: 228
TYPE: PRT
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBETITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 99806
LENGTH: 508
TYPE: PRT
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Best Local Similarity
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                                                             CVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSDLD 249
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98.7%;
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FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 68105
LENGTH: 227
TYPE: PRT
ORGANISM: pdb 1EERB
US-09-791-537-68105
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                                                                                             ; ORGANISM: pdb 1EBAA
US-09-791-537-105911
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 105911
LENGTH: 215
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Query Match
Best Local Similarity
Matches 215; Conserv
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Best Local Similarity
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 VLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSDLD 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 PPPNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLED 61
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   Conservative
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                   94.9%;
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98.2%;
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                    Score 1133; DB 5;
Pred. No. 1.7e-100;
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US-09-791-537-67299
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                                                                                                                                              Sequence 2, Application US/09502984B
GENERAL INFORMATION:
APPLICANT: Luo, Peizhi
TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES
FILE REFERENCE: A-68126-1/RFT/RMS/RMK
FILE REFERENCE: A-68126-1/RFT/RMS/RMK
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 67299
LENGTH: 213
TYPE: PRT
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Best Local
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                                    CURRENT APPLICATION NUMBER: US/09/502,984B
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/120,009
PRIOR ETILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/131,674
PRIOR FILING DATE: 1999-04-29
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APPLICANT: Debe, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                         NUMBER OF SEQ ID NOS: 37
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US-09-502-984B-18
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US-09-502-984B-2
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 86927
LENGTH: 211
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GENERAL INFORMATION
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Best Local Similarity
Matches 211; Conserv
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
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                                                                                            RLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGNGAGSVQRVEILEGRTECVLSNLRGR\\
 Application US/09502984B
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US-09-502-984B-7
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Best Local S
Matches 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09502984B GENERAL INFORMATION:
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SEQ ID NO 18
LENGTH: 211
                                                                                         Query Match
Best Local
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APPLICANT: LUO, Peizhi
TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES
FILE REFERENCE: A-68126-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/502,984B
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/120,009
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/131,674
PRIOR FILING DATE: 1999-04-29
NUMBER OF SEQ ID NOS: 37
NUMBER OF SEQ ID NOS: 37
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TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
FILE REFERENCE: A-68126-1/RFT/RMS/RMK
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/502,984B CURRENT FILING DATE: 2000-02-11
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PRIOR FILING DATE: 1999-04-29
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PRIOR FILING DATE: 1999-02-11
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                      LENGTH: 211
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                                 10 KFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRL 69
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TRYTFAVRARMAEPSFGGFWSAWSEPVSLLT 220
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                                                                       Conservative
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Pred. No. 2.4e-97;
                                                                     Score 1099; DB Pred. No. 3e-97; 4; Mismatches
                                                                                                                                                                               of Artificial Sequence: SYNTHETIC
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APPLICANT: Luo, Peizhi
TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
                                                                                                                                                                                               Sequence 13, Application US/09502984B GENERAL INFORMATION:
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Best Local Similarity
Matches 206; Conserv
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LENGTH: 211
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CURRENT APPLICATION NUMBER: US/09/502,984B
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/120,009
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/131,674
PRIOR APPLICATION NUMBER: 60/131,674
PRIOR FILING DATE: 1999-04-29
NUMBER OF SEQ ID NOS: 37
                                                                                                                                 APPLICANT: Luo, Peizhi
TITLE OF INVENTION: STRUCTURE-BASED SCREENING
FILE REFERENCE: A-68126-1/RFT/RMS/KMK
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SOFTWARE: PatentIn Ver. 2.1
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Pred. No. 4.7e-97;
5; Mismatches 0;
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US-09-502-984B-14
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GENERAL INFORMATION:
APPLICANT: Luo, Peizhi
TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES
FILE REFERENCE: A-68126-1/RFT/RMS/RMK
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/120,009
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/131,674
PRIOR FILING DATE: 1999-04-29
NUMBER OF SEQ ID NOS: 37
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                                                                       RLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGNGAGSVQRVEILEGRTECVLSNLRGR 189
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                                                     RLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGNGAGSVQRVEILEGRTECVLSNLRGR 180
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Pred. No. 5.9e-97;
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                                                                                                        NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 11
LENGTH: 211
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APPLICANT: Luo, Peizhi
APPLICANT: Luo, STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
FILE REFERENCE: A-68126-1/RFT/RMS/RMK
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SEQ ID NO 15
LENGTH: 211
                                                                                                                                                                                                                                                        APPLICANT: Luo, Peizhi
TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
FILE REFERENCE: A-68126-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/502,984B
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 05/120,009
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Best Local Similarity
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                                                                                                                                                                                            PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/131,674
PRIOR FILING DATE: 1999-04-29
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PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: 60/131,674
PRIOR FILING DATE: 1999-04-29
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                                           FEATURE:
                                                               ORGANISM: Artificial Sequence
                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TRYTFAVRARMAEPSFGGFWSAWSEPVSLLT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 TRYTFAVRARMAEPSFGGFWSAWSEPVSLLT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TRYTFAVRARMAEPSFGGFWSAWSEPVSLLT 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 KFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNFSFSFQLEDEPWKLCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HQAPTARGAVREWCSLPTADTSSEVPLELRVTAASGAPRYHRVIHINEVVLLDAPVGLVA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGNGAGSVQRVEILEGRTECVLSNLRGR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGNGAGSVQRVEILEGRTECVLSNLRGR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09502984B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                    Description of Artificial Sequence: SYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.8%;
97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.
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Pred. No. 5.9e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Query Match

91.78;

Score 1095;

DB 5;

Length 211;

Search completed: August 28, 2002, 17:39:04 Job time: 550 sec